



AKT3-5001-C1 Substitute Seq Listing.ST25  
SEQUENCE LISTING

<110> Takeda San Diego, Inc.

<120> CRYSTALLIZATION OF AKT3

<130> AKT3-5001-C1

<140> 10/601,311

<141> 2003-06-20

<150> 60/400,207

<151> 2002-07-31

<160> 4

<170> PatentIn version 3.3

<210> 1

<211> 479

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(479)

<223> Amino acid sequence for full length human wild type AKT3

<300>

<308> Genbank/NP\_005456

<309> 2002-04-04

<313> (1)..(461)

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Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp  
20 25 30

Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro  
35 40 45

Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr  
50 55 60

Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr  
65 70 75 80

Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu  
85 90 95

Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln  
100 105 110

AKT3-5001-C1 Substitute Seq Listing.ST25

Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile  
115 120 125

Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr  
130 135 140

Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly  
145 150 155 160

Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met  
165 170 175

Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His  
180 185 190

Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu  
195 200 205

Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val  
210 215 220

Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu  
225 230 235 240

Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val  
245 250 255

Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu  
260 265 270

Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr  
275 280 285

Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys  
290 295 300 305

Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp  
305 310 315 320

Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met  
325 330 335

Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu  
340 345 350

Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr  
355 360 365

AKT3-5001-C1 Substitute Seq Listing.ST25

Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp  
370 375 380

Pro Asn Lys Arg Leu Gly Gly Pro Asp Asp Ala Lys Glu Ile Met  
385 390 395 400

Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys  
405 410 415

Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr  
420 425 430

Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro  
435 440 445

Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg  
450 455 460

Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu  
465 470 475

<210> 2  
<211> 978  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(978)  
<223> Human cDNA sequence encoding residues 136-461 of AKT3

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aaaggcactt ttggaaagt tattttgtt cgagagaagg caagtggaaa atactatgct 120  
atgaagattc tgaagaaaga agtcattatt gcaaaggatg aagtggcaca cactctaact 180  
gaaaggcagag tattaaagaa cactagacat cccttttaa catccttgaa atattccttc 240  
cagacaaaag accgtttgtg ttttgtatg gaatatgtt atggggcgaa gctgttttc 300  
catttgtcga gagagcgggt gttctctgag gaccgcacac gtttctatgg tgcagaaatt 360  
gtctctgcct tggactatct acattccgga aagattgtgt accgtatct caagttggag 420  
aatctaatgc tggacaaaga tggccacata aaaattacag atttggact ttgcaaagaa 480  
gggatcacag atgcagccac catgaagaca ttctgtggca ctccagaata tctggcacca 540  
gaggtgttag aagataatga ctatggccga gcagtagact ggtggggcct aggggttgc 600  
atgtatgaaa tgatgtgtgg gaggttacct ttctacaacc aggaccatga gaaactttt 660

AKT3-5001-C1 Substitute Seq Listing.ST25

gaattaatat	taatggaga	cattaaat	ttcgaacac	tctttcaga	tgcaaaatca	720
ttgcttcag	ggctcttgc	aaaggatcca	aataaacgcc	ttggggagg	accagatgtat	780
gcaaaagaaa	ttatgagaca	cagttcttc	tctggagtaa	actggcaaga	tgtatatgtat	840
aaaaagcttgc	accccttt	taaacctcaa	gtaacatctg	agacagatac	tagatat	900
gatgaagaat	ttacagctca	gactattaca	ataacaccac	ctgaaaaata	tgtgaggat	960
ggtaggact	gcatggac					978

<210> 3  
<211> 556  
<212> PRT  
<213> Artificial

<220>  
<223> Amino acid sequence for residues 136-461 of AKT3 with a cleavable  
intein tag and cleavage site

<220>  
<221> MISC\_FEATURE  
<222> (1)..(226)  
<223> Cleavable N-terminal intein tag

<220>  
<221> MISC\_FEATURE  
<222> (227)..(230)  
<223> CRSL cleavage site

<220>  
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<222> (231)..(556)  
<223> Amino acid sequence for residues 136-461 of AKT3

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Met Lys Ile Glu Glu Gly Lys Leu Thr Asn Pro Gly Val Ser Ala Trp  
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Gln Val Asn Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly  
20 25 30

Lys Thr Tyr Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu  
35 40 45

Pro Ser Asn Val Pro Ala Leu Trp Gln Leu Gln Asn Asn Gly Asn Asn  
50 55 60

Gly Leu Glu Leu Arg Glu Ser Gly Ala Ile Ser Gly Asp Ser Leu Ile  
65 70 75 80

Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp  
85 90 95

AKT3-5001-C1 Substitute Seq Listing.ST25

Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu  
100 105 110

Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val  
115 120 125

Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn  
130 135 140

His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser  
145 150 155 160

Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu  
165 170 175

Gln Leu Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile Tyr Trp  
180 185 190

Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val Phe Asp  
195 200 205

Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile Ile Val  
210 215 220

His Asn Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met  
225 230 235 240

Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys  
245 250 255

Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys  
260 265 270

Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr  
275 280 285

Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr  
290 295 300

Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met  
305 310 315 320

Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg  
325 330 335

Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser  
Page 5

AKT3-5001-C1 Substitute Seq Listing.ST25

340 345 350

Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys  
355 360 365

Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp  
370 375 380

Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr  
385 390 395 400

Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn  
405 410 415

Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr  
420 425 430

Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys  
435 440 445

Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu  
450 455 460

Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro  
465 470 475 480

Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg  
485 490 495

His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys  
500 505 510

Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg  
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Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro  
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Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp  
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<210> 4  
<211> 330  
<212> PRT  
<213> Artificial

<220>  
<223> CRSL fused to the N-terminal of amino acid residues 136-461 of AKT3

AKT3-5001-C1 Substitute Seq Listing.ST25

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<223> CRSL cleavage site

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Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile  
20 25 30

Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys Ile Leu  
35 40 45

Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr Leu Thr  
50 55 60

Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr Ser Leu  
65 70 75 80

Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met Glu Tyr  
85 90 95

Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe  
100 105 110

Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu  
115 120 125

Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys Leu Glu  
130 135 140

Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly  
145 150 155 160

Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr Phe Cys  
165 170 175

Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr  
180 185 190

Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met  
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195

200

205

Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe  
210 215 220

Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu Ser Ser  
225 230 235 240

Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro Asn Lys  
245 250 255

Arg Leu Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg His Ser  
260 265 270

Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys Leu Val  
275 280 285

Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe  
290 295 300

Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro Glu Lys  
305 310 315 320

Tyr Asp Glu Asp Gly Met Asp Cys Met Asp  
325 330

AKT3-5001-C1 Substitute Seq Listing.ST25  
SEQUENCE LISTING

<110> Takeda San Diego, Inc.

<120> CRYSTALLIZATION OF AKT3

<130> AKT3-5001-C1

<140> 10/601,311

<141> 2003-06-20

<150> 60/400,207

<151> 2002-07-31

<160> 4

<170> PatentIn version 3.3

<210> 1

<211> 479

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(479)

<223> Amino acid sequence for full length human wild type AKT3

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<308> Genbank/NP\_005456

<309> 2002-04-04

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Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp  
20 25 30

Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro  
35 40 45

Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr  
50 55 60

Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr  
65 70 75 80

Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu  
85 90 95

Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln  
100 105 110

AKT3-5001-C1 Substitute Seq Listing.ST25

Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile  
115 120 125

Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr  
130 135 140

Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly  
145 150 155 160

Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met  
165 170 175

Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His  
180 185 190

Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu  
195 200 205

Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val  
210 215 220

Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu  
225 230 235 240

Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val  
245 250 255

Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu  
260 265 270

Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr  
275 280 285

Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys  
290 295 300

Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp  
305 310 315 320

Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met  
325 330 335

Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu  
340 345 350

Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr  
355 360 365

AKT3-5001-C1 Substitute Seq Listing.ST25

Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp  
370 375 380

Pro Asn Lys Arg Leu Gly Gly Pro Asp Asp Ala Lys Glu Ile Met  
385 390 395 400

Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys  
405 410 415

Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr  
420 425 430

Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro  
435 440 445

Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg  
450 455 460

Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu  
465 470 475

<210> 2  
<211> 978  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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atgaagattc tgaagaaaga agtcattatt gcaaaggatg aagtggcaca cactctaact 180  
gaaagcagag tattaaagaa cactagacat cccttttaa catcctgaa atattccttc 240  
cagacaaaag accgttgtg ttttgtatg gaatatgtt aatggggcgaa gctgttttc 300  
catttgtcga gagagcgggt gttctctgag gaccgcacac gtttctatgg tgcagaaatt 360  
gtctctgcct tggactatct acattccgga aagattgtgt accgtgatct caagttggag 420  
aatctaattgc tggacaaaga tggccacata aaaattacag attttggact ttgcaaagaa 480  
gggatcacag atgcagccac catgaagaca ttctgtggca ctccagaata tctggcacca 540  
gaggtgttag aagataatga ctatggccga gcagtagact ggtggggcct aggggttgc 600  
atgtatgaaa tgatgtgtgg gaggttacct ttctacaacc aggaccatga gaaactttt 660

AKT3-5001-C1 Substitute Seq Listing.ST25

gaattaatat taatggaaga cattaaattt cctcgaacac tctcttcaga tgcaaaaatca 720  
ttgcgttcag ggctcttgat aaaggatcca aataaacgcc ttggggagg accagatgat 780  
gcaaaaagaaa ttatgagaca cagttcttc tctggagtaa actggcaaga tgtatatgat 840  
aaaaagcttg taccccttt taaacctcaa gtaacatctg agacagatac tagatatttt 900  
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<210> 3  
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<212> PRT  
<213> Artificial

<220>  
<223> Amino acid sequence for residues 136-461 of AKT3 with a cleavable  
intein tag and cleavage site

<220>  
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<223> CRSL cleavage site

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<223> Amino acid sequence for residues 136-461 of AKT3

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Met Lys Ile Glu Glu Gly Lys Leu Thr Asn Pro Gly Val Ser Ala Trp  
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Gln Val Asn Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly  
20 25 30

Lys Thr Tyr Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu  
35 40 45

Pro Ser Asn Val Pro Ala Leu Trp Gln Leu Gln Asn Asn Gly Asn Asn  
50 55 60

Gly Leu Glu Leu Arg Glu Ser Gly Ala Ile Ser Gly Asp Ser Leu Ile  
65 70 75 80

Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp  
85 90 95

AKT3-5001-C1 Substitute Seq Listing.ST25

Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu  
100 105 110

Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val  
115 120 125

Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn  
130 135 140

His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser  
145 150 155 160

Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu  
165 170 175

Gln Leu Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile Tyr Trp  
180 185 190

Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val Phe Asp  
195 200 205

Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile Ile Val  
210 215 220

His Asn Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met  
225 230 235 240

Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys  
245 250 255

Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys  
260 265 270

Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr  
275 280 285

Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr  
290 295 300

Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met  
305 310 315 320

Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg  
325 330 335

Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser  
Page 5

AKT3-5001-C1 Substitute Seq Listing.ST25

340                    345                    350

Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys  
355 360 365

Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp  
370 375 380

Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr  
385 390 395 400

Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn  
405 410 415

Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr  
420 425 430

Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys  
435 440 445

Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu  
450 455 460

Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro  
465 470 475 480

Asn Lys Arg Leu Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg  
485 490 495

His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys  
500 505 510

Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg  
515 520 525

Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro  
530 535 540 .

Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp  
545 550 555

<210> 4  
<211> 330  
<212> PRT  
<213> Artificial

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<223> CRSL fused to the N-terminal of amino acid residues 136-461 of AKT3

AKT3-5001-C1 Substitute Seq Listing.ST25

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<222> (1)..(4)  
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<220>  
<221> MISC\_FEATURE  
<222> (5)..(330)  
<223> Amino acid sequence for residues 136-461 of AKT3

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Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met Asn Asp  
1 5 10 15

Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile  
20 25 30

Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys Ile Leu  
35 40 45

Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr Leu Thr  
50 55 60

Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr Ser Leu  
65 70 75 80

Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met Glu Tyr  
85 90 95

Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe  
100 105 110

Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu  
115 120 125

Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys Leu Glu  
130 135 140

Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly  
145 150 155 160

Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr Phe Cys  
165 170 175

Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr  
180 185 190

Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met  
Page 7

195

AKT3-5001-C1 Substitute Seq Listing.ST25  
200                   205

Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe  
210                   215                   220

Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu Ser Ser  
225                   230                   235                   240

Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro Asn Lys  
245                   250                   255

Arg Leu Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg His Ser  
260                   265                   270

Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys Leu Val  
275                   280                   285

Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe  
290                   295                   300

Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro Glu Lys  
305                   310                   315                   320

Tyr Asp Glu Asp Gly Met Asp Cys Met Asp  
325                   330